B68 Assessment of Hair Roots for Nuclear DNA Analysis

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After attending this presentation, attendees will learn how to effec- tively determine whether or not a hair root will yield a DNA STR profile.

This presentation will impact the forensic community and/or humanity by potential saving time and money by correctly identifying whether or not a hair root will yield a DNA STr profile prior to attempting the analysis

This presentation will outline the results of a study, whose purpose was to evaluate the accessibility of nuclear DNA of hair roots in the catagen/telogen transition growth stages. Morphological characteristics were assessed to determine cost effective screening of hair root suitability for nuclear DNA analysis.

Hairs proceed through a growth cycle consisting of three phases: anagen, catagen and telogen. Determination of the phase of a hair's growth cycle is used to assess the suitability of the hair root for nuclear DNA analysis. Hair roots in the actively growing anagen phase are an excellent source of nuclear DNA, while hair roots in the resting telogen phase lack sufficient nuclear DNA. The likelihood of obtaining nuclear DNA declines in the catagen phase as the hair nears the telogen phase, thereupon increasing the reliance on mitochondrial DNA analysis.

The morphological characteristics of roots belonging to the anagen and telogen phases are readily identifiable, as the typical ribbon root and club root. However, the morphological characteristics of roots in the tran- sition from the anagen phase to the catagen phase and into the telogen phase, are not. The Centre of Forensic Sciences (CFS) has yet to establish an effective screening method for determining the accessibility of nuclear DNA analysis of those hair roots. This has led to a costly hit and miss sce- nario, whereby, a root may or may not provide sufficient nuclear DNA for analysis.

This study examined scalp hair roots in the transition from the anagen phase to the catagen phase and into the telogen phase. Specifically, roots were chosen with club roots that had folicular tags and partial club roots with germinal nipples. Various morphological characteristics were mea- sured to determine if there was a correlation with amount of nuclear DNA obtainable. The hair shaft width, and the length and width of the club root, germinal nipple and folicular tag were measured employing a stereoscopic microscope with calibrated graticule in one eyepiece at magnifications of 40x to 100x. These roots were subjected to nuclear DNA analysis. The quantity of nuclear DNA obtained and resulting DNA profiles were assessed.

A sample of 51 hair roots were measured and analyzed. The sample contained 34 club roots with germinal nipples and 17 club roots with folicular tags. The majority of the hair roots (n=40, 78.4%) did not have sufficient nuclear DNA to proceed with amplification (minimum threshold 240pg). Six club roots with germinal nipples did proceed on to amplifi- cation and four generated profiles. Five club roots with folicular tags also processed for amplification and three generated profiles. Therefore, 11.8% of club roots with germinal nipples gave profiles and 17.6% of club roots with folicular tags. No linear correlation was seen between the morpho- logical dimensions measured and amount of nuclear DNA obtained. However, it is of note that DNA profiles were only obtained in germinal nipples longer than 132µm and in folicular tags longer than 30µm.

Based on this study, the expectation of obtaining nuclear DNA from a catagen/telogen root with a germinal nipple or folicular tag is low, but mea- suring the length of germinal nipples or folicular tags may be useful in determining the likelihood of obtaining sufficient nuclear DNA.

Hair Root, Screening Method, Morphological Characteristics

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